PATENT
Docket No.: **2283/301**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant :	Leivan DeVeylder et al	Examiner: C. Collins
Serial No. :	09/574,735	Art Unit: 1638
Conf. No. :	1507	
Filed :	May 18, 2000	
For :	CYCLIN-DEPENDENT KINASE INHIBITORS AND USES THEREOF	

STATEMENT UNDER 37 C.F.R. § 1.825(a) AND (b)

Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

I hereby state that support for the substitute paper copy of the Sequence Listing exists in the above-captioned application as originally filed. The substitute paper copy of the Sequence Listing submitted herewith does not add new matter to the application as originally filed. In addition, the information recorded in the substitute computer readable form (CRF) of the Sequence Listing submitted herewith, is identical to the information contained in the substitute paper copy of the Sequence Listing.

Respectfully submitted,

Dated: October 12, 2001

Ann R. Pokalsky
Registration No. 34,697

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ARP/mm

G201614.1

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I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231, on the date below.

10/12/01 | Maria Matos
Date | Maria Matos

Application No.: 09/574735

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
Technical Assistance.....703-287-0200
To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

#19

SEQUENCE LISTING

<110> De Veylder, Lieven
Beeckman, Tom
Inzé, Dirk
Van Camp, Wim
Krols, Luc

<120> Cyclin-dependent kinase inhibitors and uses thereof

<130> 2283/301

<140> US 09/574,735
<141> 2000-05-18

<160> 48

<170> PatentIn version 3.0

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<222> (86)..(712)

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                              1               5
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Asp Val Val Glu Glu Asn Gly Val Thr Thr Thr Thr Val Lys Arg Arg
10                  15                  20                  25
aag atg gag gag gaa gtg gat tta gtg gaa tct agg ata att ctg tct      208
Lys Met Glu Glu Glu Val Asp Leu Val Glu Ser Arg Ile Ile Leu Ser
                30                  35                  40
ccg tgt gta cag gcg acg aat cgc ggt gga att gtg gcg aga aat tca      256
Pro Cys Val Gln Ala Thr Asn Arg Gly Gly Ile Val Ala Arg Asn Ser
            45                  50                  55
gca gga gcg tcg gag acg agt gtt gtt ata gta cga cgg cga gat tct      304
Ala Gly Ala Ser Glu Thr Ser Val Val Ile Val Arg Arg Arg Asp Ser
        60                  65                  70
cct ccg gtt gaa gaa cag tgt caa atc gaa gaa gaa gat tcg tcg gtt      352
Pro Pro Val Glu Glu Gln Cys Gln Ile Glu Glu Glu Asp Ser Ser Val
    75                  80                  85
tcg tgt tgt tct aca tcg gaa gag aaa tcg aaa cgg aga atc gaa ttt      400
Ser Cys Cys Ser Thr Ser Glu Glu Lys Ser Lys Arg Arg Ile Glu Phe
90                  95                  100                 105
gta gat ctt gag gaa aat aac ggt gac gat cgt gaa aca gaa acg tcg      448
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tgg att tac gat gat ttg aat aag agt gag gaa tcg atg aac atg gat      496
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            125                 130                 135
tct tct tcg gtg gct gtt gaa gat gta gag tct cgc cgc agg tta agg      544
Ser Ser Ser Val Ala Val Glu Asp Val Glu Ser Arg Arg Arg Leu Arg
        140                 145                 150
aag agt ctc cat gag acg gtg aag gaa gct gag tta gaa gat ttt ttt      592
Lys Ser Leu His Glu Thr Val Lys Glu Ala Glu Leu Glu Asp Phe Phe
    155                 160                 165
cag gtg gcg gag aaa gat ctt cgg aat aag ttg ttg gaa tgt tct atg      640
Gln Val Ala Glu Lys Asp Leu Arg Asn Lys Leu Leu Glu Cys Ser Met
170                 175                 180                 185
aag tat aac ttc gat ttc gag aaa gat gag cca ctt ggt gga gga aga      688
Lys Tyr Asn Phe Asp Phe Glu Lys Asp Glu Pro Leu Gly Gly Gly Arg
                190                 195                 200
tac gag tgg gtt aaa ttg aat cca tgaagaagac gatgatgata atgatgatca     742
Tyr Glu Trp Val Lys Leu Asn Pro
            205
ttgttttcac caaagtactt attatttttc ttctgtaata atctttgctt tgatttttct    802
tttaacaaaa tccaaatgta gatatctttc tctcgaataa tcaataacat gtaattcaac    862
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<210> 2
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<400> 2

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            20                  25                  30
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        35                  40                  45
Arg Gly Gly Ile Val Ala Arg Asn Ser Ala Gly Ala Ser Glu Thr Ser
    50                  55                  60
Val Val Ile Val Arg Arg Arg Asp Ser Pro Pro Val Glu Glu Gln Cys
65                  70                  75                  80
Gln Ile Glu Glu Glu Asp Ser Ser Val Ser Cys Cys Ser Thr Ser Glu
                85                  90                  95
Glu Lys Ser Lys Arg Arg Ile Glu Phe Val Asp Leu Glu Glu Asn Asn
            100                 105                 110
Gly Asp Asp Arg Glu Thr Glu Thr Ser Trp Ile Tyr Asp Asp Leu Asn
        115                 120                 125
Lys Ser Glu Glu Ser Met Asn Met Asp Ser Ser Ser Val Ala Val Glu
    130                 135                 140
Asp Val Glu Ser Arg Arg Arg Leu Arg Lys Ser Leu His Glu Thr Val
145                 150                 155                 160
Lys Glu Ala Glu Leu Glu Asp Phe Phe Gln Val Ala Glu Lys Asp Leu
                165                 170                 175
Arg Asn Lys Leu Leu Glu Cys Ser Met Lys Tyr Asn Phe Asp Phe Glu
            180                 185                 190
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Ser Lys Ala Thr Ala Pro Ser Pro Gly Val Arg Thr Arg Ala Ala Lys
    15                  20                  25
acc cta gcc ttg aag cgg ctt aat tcc tcc gcc gct gat tca gct cta       145
Thr Leu Ala Leu Lys Arg Leu Asn Ser Ser Ala Ala Asp Ser Ala Leu
30                  35                  40                  45
cct aac gac tct tct tgc tat ctt cag ctc cgt agc cgc cgt ctc gag       193
Pro Asn Asp Ser Ser Cys Tyr Leu Gln Leu Arg Ser Arg Arg Leu Glu
                50                  55                  60
aaa ccc tct tcg ctg att gaa ccg aaa cag ccg ccg aga gtt cac aga       241
Lys Pro Ser Ser Leu Ile Glu Pro Lys Gln Pro Pro Arg Val His Arg
            65                  70                  75
tcg gga att aaa gag tct ggt tcc agg tct cgc gtt gac tcg gtt aac       289
Ser Gly Ile Lys Glu Ser Gly Ser Arg Ser Arg Val Asp Ser Val Asn
        80                  85                  90
tcg gtt cct gta gct cag agc tct aat gaa gat gaa tgt ttt gac aat       337
Ser Val Pro Val Ala Gln Ser Ser Asn Glu Asp Glu Cys Phe Asp Asn
    95                  100                 105
ttc gtg agt gtc caa gtt tct tgt ggt gaa aac agt ctc ggt ttt gaa       385
Phe Val Ser Val Gln Val Ser Cys Gly Glu Asn Ser Leu Gly Phe Glu
110                 115                 120                 125
tca aga cac agc aca agg gag agc acg cct tgt aac ttt gtt gag gat       433
Ser Arg His Ser Thr Arg Glu Ser Thr Pro Cys Asn Phe Val Glu Asp
                130                 135                 140
atg gag atc atg gtt aca cca ggg tct agc acg agg tcg atg tgc aga       481
Met Glu Ile Met Val Thr Pro Gly Ser Ser Thr Arg Ser Met Cys Arg
            145                 150                 155
gca acc aaa gag tac aca agg gaa caa gat aac gtg atc ccg acc act       529
Ala Thr Lys Glu Tyr Thr Arg Glu Gln Asp Asn Val Ile Pro Thr Thr
        160                 165                 170
agt gaa atg gag gag ttc ttt gca tat gca gag cag cag caa cag agg       577
Ser Glu Met Glu Glu Phe Phe Ala Tyr Ala Glu Gln Gln Gln Gln Arg
    175                 180                 185
cta ttc atg gag aag tac aac ttc gac att gtg aat gat atc ccc ctc       625
Leu Phe Met Glu Lys Tyr Asn Phe Asp Ile Val Asn Asp Ile Pro Leu
190                 195                 200                 205
agc gga cgt tac gaa tgg gtg caa gtc aaa cca tgaagttcaa aaggaaacag     678
Ser Gly Arg Tyr Glu Trp Val Gln Val Lys Pro
                210                 215
ctccaaaaga catggtgtga agttagagaa tgtgatggag ttaacagact aaccaaacat     738
cagaaatcgt gtaatcttaa gtaataatgt ggttagagaa caagtttgag agtagcttag     798
ggaccttaaa acctcacacc atttgtaata ctaatcttct tcagatgctt agtgaaattt     858
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<213> Arabidopsis thaliana

<400> 4

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        35                  40                  45
Ser Ala Leu Pro Asn Asp Ser Ser Cys Tyr Leu Gln Leu Arg Ser Arg
    50                  55                  60
Arg Leu Glu Lys Pro Ser Ser Leu Ile Glu Pro Lys Gln Pro Pro Arg
65                  70                  75                  80
Val His Arg Ser Gly Ile Lys Glu Ser Gly Ser Arg Ser Arg Val Asp
                85                  90                  95
Ser Val Asn Ser Val Pro Val Ala Gln Ser Ser Asn Glu Asp Glu Cys
            100                 105                 110
Phe Asp Asn Phe Val Ser Val Gln Val Ser Cys Gly Glu Asn Ser Leu
        115                 120                 125
Gly Phe Glu Ser Arg His Ser Thr Arg Glu Ser Thr Pro Cys Asn Phe
    130                 135                 140
Val Glu Asp Met Glu Ile Met Val Thr Pro Gly Ser Ser Thr Arg Ser
145                 150                 155                 160
Met Cys Arg Ala Thr Lys Glu Tyr Thr Arg Glu Gln Asp Asn Val Ile
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Pro Thr Thr Ser Glu Met Glu Glu Phe Phe Ala Tyr Ala Glu Gln Gln
            180                 185                 190
Gln Gln Arg Leu Phe Met Glu Lys Tyr Asn Phe Asp Ile Val Asn Asp
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Ile Pro Leu Ser Gly Arg Tyr Glu Trp Val Gln Val Lys Pro
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<213> Arabidopsis thaliana

<220>
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                                    Met Gly Lys Tyr Met Lys Lys
                                    1               5
ctc aaa tcc aaa tca gaa tct cct tca ccc aat tca aca cca aca cca      160
Leu Lys Ser Lys Ser Glu Ser Pro Ser Pro Asn Ser Thr Pro Thr Pro
        10                  15                  20
tca cca tca cca tca cca aca cca atc acc acc aat tca cca cca cca      208
Ser Pro Ser Pro Ser Pro Thr Pro Ile Thr Thr Asn Ser Pro Pro Pro
    25                  30                  35
aca aca ccc aat tcc tct gat ggt gtt cga act cgt gct aga acc cta      256
Thr Thr Pro Asn Ser Ser Asp Gly Val Arg Thr Arg Ala Arg Thr Leu
40                  45                  50                  55
gct ttg gag aat tcc aac aat cag aat cag aat ctt tct gtt tct tct      304
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                60                  65                  70
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Asp Ser Tyr Leu Gln Leu Arg Asn Arg Arg Leu Lys Arg Pro Leu Ile
            75                  80                  85
agg caa cat tcc gct aag agg aat aag ggg cat gat gga aac cct aaa      400
Arg Gln His Ser Ala Lys Arg Asn Lys Gly His Asp Gly Asn Pro Lys
        90                  95                  100
tcc cca att ggg gat tca att gct gaa gag aaa act gtt cag aag agt      448
Ser Pro Ile Gly Asp Ser Ile Ala Glu Glu Lys Thr Val Gln Lys Ser
    105                 110                 115
cct gag cct gaa aat gct gaa ttc aag gag aat gct gag gat act gag      496
Pro Glu Pro Glu Asn Ala Glu Phe Lys Glu Asn Ala Glu Asp Thr Glu
120                 125                 130                 135
aga agc gct agg gaa act aca ccc gtc cat ttg ata atg cga gca gac      544
Arg Ser Ala Arg Glu Thr Thr Pro Val His Leu Ile Met Arg Ala Asp
                140                 145                 150
gtt ctc agg cct cct agg cca att acc agg cgt act ttt cca act gaa      592
Val Leu Arg Pro Pro Arg Pro Ile Thr Arg Arg Thr Phe Pro Thr Glu
            155                 160                 165
gct aat ccc aaa acg gag cag cca act atc cca att tca cgc gaa ttt      640
Ala Asn Pro Lys Thr Glu Gln Pro Thr Ile Pro Ile Ser Arg Glu Phe
        170                 175                 180
gag gaa ttc tgt gct aaa cat gaa gcc gag cag caa agg gag ttc atg      688
Glu Glu Phe Cys Ala Lys His Glu Ala Glu Gln Gln Arg Glu Phe Met
    185                 190                 195
gag aag tac aac ttt gat cct gtg aca gag cag cca ctc cca ggg cgt      736
Glu Lys Tyr Asn Phe Asp Pro Val Thr Glu Gln Pro Leu Pro Gly Arg
200                 205                 210                 215
tac gaa tgg gaa aaa gtg tcg ccc tag aaggcaggct agtattaagt            783
Tyr Glu Trp Glu Lys Val Ser Pro
                220
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tgctatttcc attttccatc actttctatt tacttgtaaa gaaagtagga ctttcaacat    903
atgtagacta atgatctgta actttacaga ggtgttgatt acacaacaat acaaagtcct    963
ttgtctagca gatcattaaa gaagggtttg agggaataag ggtctctagt tgtagggttt   1023
agggtataaa atcaaagtag ggtatgtaag agaggtttta caagaatttc cttttgttct   1083
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<213> Arabidopsis thaliana

<400> 6

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        35                  40                  45
Arg Thr Arg Ala Arg Thr Leu Ala Leu Glu Asn Ser Asn Asn Gln Asn
    50                  55                  60
Gln Asn Leu Ser Val Ser Ser Asp Ser Tyr Leu Gln Leu Arg Asn Arg
65                  70                  75                  80
Arg Leu Lys Arg Pro Leu Ile Arg Gln His Ser Ala Lys Arg Asn Lys
                85                  90                  95
Gly His Asp Gly Asn Pro Lys Ser Pro Ile Gly Asp Ser Ile Ala Glu
            100                 105                 110
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Glu Lys Thr Val Gln Lys Ser Pro Glu Pro Glu Asn Ala Glu Phe Lys
        115                 120                 125
Glu Asn Ala Glu Asp Thr Glu Arg Ser Ala Arg Glu Thr Thr Pro Val
    130                 135                 140
His Leu Ile Met Arg Ala Asp Val Leu Arg Pro Pro Arg Pro Ile Thr
145                 150                 155                 160
Arg Arg Thr Phe Pro Thr Glu Ala Asn Pro Lys Thr Glu Gln Pro Thr
                165                 170                 175
Ile Pro Ile Ser Arg Glu Phe Glu Glu Phe Cys Ala Lys His Glu Ala
            180                 185                 190
Glu Gln Gln Arg Glu Phe Met Glu Lys Tyr Asn Phe Asp Pro Val Thr
        195                 200                 205
Glu Gln Pro Leu Pro Gly Arg Tyr Glu Trp Glu Lys Val Ser Pro
    210                 215                 220
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<220>
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<210> 11
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<210> 14
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<220>
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<400> 14
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<210> 15
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<220>
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<210> 33
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<212> PRT
<213> Arabidopsis thaliana

<220>
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<222> (5)
<223> Xaa at postiion 5 may be Asp or Glu

<220>
<221> UNSURE
<222> (6)..(8)
<223> Xaa at any of positions 6, 7 or 8 may be any amino acid

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1 5 10

<210> 34
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<220>
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<222> (2)..(3)
<223> Xaa at positions 2 and 3 may be any amino acid

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Phe Xaa Xaa Lys Tyr Asn Phe Asp
1 5

<210> 35
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<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (1)
<223> Xaa at position 1 may be Pro or Leu

<220>
<221> UNSURE
<222> (3)
<223> Xaa at position 3 may be any amino acid

<400> 35
Xaa Leu Xaa Gly Arg Tyr Glu Trp
1 5

<210> 36
<211> 10
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (2)
<223> Xaa at position 2 may be any amino acid

<220>
<221> UNSURE
<222> (4)
<223> Xaa at position 4 may be Asp or Glu

<220>
<221> UNSURE
<222> (7)..(9)
<223> Xaa at positions 7, 8 or 9 may be any amino acid

<400> 36
Glu Xaa Glu Xaa Phe Phe Xaa Xaa Xaa Glu
1 5 10

<210> 37
<211> 8
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (2)
<223> Xaa at position 2 may be any amino acid

<400> 37
Tyr Xaa Gln Leu Arg Ser Arg Arg
1 5

<210> 38
<211> 9
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (5)
<223> Xaa at position 5 may be Met or Ile

<220>
<221> UNSURE
<222> (6)
<223> Xaa at position 6 may be Lys or Arg

<220>
<221> UNSURE
<222> (8)
<223> Xaa at position 8 may be any amino acid

<220>
<221> UNSURE
<222> (9)
<223> Xaa at position 9 may be Lys or Arg

<400> 38
Met Gly Lys Tyr Xaa Xaa Lys Xaa Xaa
1 5

<210> 39
<211> 8
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (2)
<223> Xaa at position 2 may be any amino acid

<400> 39
Ser Xaa Gly Val Arg Thr Arg Ala
1 5

<210> 40
<211> 327
<212> PRT
<213> Arabidopsis thaliana

<400> 40
Met Gly Lys Tyr Ile Arg Lys Ser Lys Ile Asp Gly Ala Gly Ala Gly
1 5 10 15
Ala Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ser Ser Ile Ala
20 25 30
Leu Met Asp Val Val Ser Pro Ser Ser Ser Ser Ser Leu Gly Val Leu
35 40 45
Thr Arg Ala Lys Ser Leu Ala Leu Gln Gln Gln Gln Gln Arg Cys Leu
50 55 60

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Leu Gln Lys Pro Ser Ser Pro Ser Ser Leu Pro Pro Thr Ser Ala Ser
65                  70                  75                  80
Pro Asn Pro Pro Ser Lys Gln Lys Met Lys Lys Lys Gln Gln Gln Met
                85                  90                  95
Asn Asp Cys Gly Ser Tyr Leu Gln Leu Arg Ser Arg Arg Leu Gln Lys
            100                 105                 110
Lys Pro Pro Ile Val Val Ile Arg Ser Thr Lys Arg Arg Lys Gln Gln
        115                 120                 125
Arg Arg Asn Glu Thr Cys Gly Arg Asn Pro Asn Pro Arg Ser Asn Leu
    130                 135                 140
Asp Ser Ile Arg Gly Asp Gly Ser Arg Ser Asp Ser Val Ser Glu Ser
145                 150                 155                 160
Val Val Phe Gly Lys Asp Lys Asp Leu Ile Ser Glu Ile Asn Lys Asp
                165                 170                 175
Pro Thr Phe Gly Gln Asn Phe Phe Asp Leu Glu Glu Glu His Thr Gln
            180                 185                 190
Ser Phe Asn Arg Thr Thr Arg Glu Ser Thr Pro Cys Ser Leu Ile Arg
        195                 200                 205
Arg Pro Glu Ile Met Thr Thr Pro Gly Ser Ser Thr Lys Leu Asn Ile
    210                 215                 220
Cys Val Ser Glu Ser Asn Gln Arg Glu Asp Ser Leu Ser Arg Ser His
225                 230                 235                 240
Arg Arg Arg Pro Thr Thr Pro Glu Met Asp Glu Phe Phe Ser Gly Ala
                245                 250                 255
Glu Glu Glu Gln Gln Lys Gln Phe Ile Glu Lys Tyr Val Phe Pro Arg
            260                 265                 270
Phe Ile Cys Ser Val Leu Leu Val Met Ser Phe Gln Phe Val Leu Phe
        275                 280                 285
Phe Ser Phe Gly Leu Val Ser Leu Met Val Ser Val Asn Ser Phe Phe
    290                 295                 300
Arg Tyr Asn Phe Asp Pro Val Asn Glu Gln Pro Leu Pro Gly Arg Phe
305                 310                 315                 320
Glu Trp Thr Lys Val Asp Asp
                325
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<210> 41
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe or Primer

<400> 41
agaccatggc ggcggttagg ag 22

<210> 42
<211> 12
<212> PRT
<213> Tag·100 epitope

<400> 42
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1               5                   10
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<210> 43
<211> 10
<212> PRT
<213> c-myc epitope

<400> 43
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1 5 10

<210> 44
<211> 7
<212> PRT
<213> FLAG-epitope

<400> 44
Asp Tyr Lys Asp Asp Asp Lys
1 5

<210> 45
<211> 9
<212> PRT
<213> HA-epitope

<400> 45
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 46
<211> 12
<212> PRT
<213> protein C epitope

<400> 46
Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys
1 5 10

<210> 47
<211> 11
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<213> VSV epitope

<400> 47
Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
1 5 10

<210> 48
<211> 9
<212> DNA
<213> Escherichia coli

<400> 48
agg aga aga 12
Arg Arg Arg
1